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[illegible]

1 AGACACCTCT GCCCTCACCA TGAGCCTCTG GCAGCCCCTG GTCCTGGTGC TCCTGGTGCT  
61 GGGCTGCTGC TTTGCTGCCC CCAGACAGCG CCAGTCCACC CTTGTGCTCT TCCCTGGAGA  
121 CCTGAGAACC AATCTCACCG ACAGGCAGCT GGCAGAGGAA TACCTGTACC GCTATGGTTA  
181 CACTCGGGTG GCAGAGATGC GTGGAGAGTC GAAATCTCTG GGGCCTGCGC TGCTGCTTCT  
241 CCAGAAGCAA CTGTCCCTGC CCGAGACCAG TGAGCTGGAT AGCGCCACGC TGAAGGCCAT  
301 GCGAACCCCA CGGTGCGGGG TCCCAGACCT GGGCAGATTG CAAACCTTTG AGGGCGACCT  
361 CAAGTGGCAC CACCACAACA TCACCTATTG GATCCAAAAC TACTCGGAAG ACTTGCCGCG  
421 GCGGTGATT GACGACGCTT TTGCCGCGC CTTGCACTG TGGAGCGCGG TGACGCCGCT  
481 CACCTTCACT CGCGTGACA GCCGGGACGC AGACATCGTC ATCCAGTTTG GTGTCGCGGA  
541 GCACGGAGAC GGGTATCCCT TCGACGGGAA GGACGGGCTC CTGGCACACG CCTTTCCTCC  
601 TGGCCCCGGC ATTACGGGAG ACGCCCATTT CGACGATGAC GAGTTGTGGT CCCTGGGCAA  
661 GGCGTCTGTG GTTCCAATC GGTTTGGAAA CGCAGATGGC GCGGCCTGCC ACTTCCCCTT  
721 CATCTTCGAG GGCGCTCCT ACTCTGCCTG CACCACCGAC GGTGCTCCG ACGGGTTGCC  
781 CTGGTGCAGT ACCACGGCCA ACTACGACAC CGACGACCGG TTTGGCTTCT GCGCCAGCGA  
841 GAGACTCTAC ACCCGGGACG GCAATGCTGA TGGGAAACCC TGCCAGTTTC CATTATCTT  
901 CCAAGGCCAA TCCTACTCCG CTGCAACCAC GGACGGTCGC TCCGACGGCT ACCGCTGGTG  
961 GCCCAACCACC GCCAATACG ACCGGGACAA GCTCTTCGGC TTCTGCCCGA CCCGAGCTGA  
1021 CTCGACGGTG ATGGGGGGCA ACTCGGCGGG GGAGCTGTGC GTCTTCCCCT TCACTTTCCT  
1081 GGGTAAGGAG TACTCGACCT GTACCAGCGA GGGCCGCGGA GATGGGCGCC TCTGGTGGCG  
1141 TACCACCTCG AACTTTGACA GCGACAAGAA GTGGGGCTTC TGCCCGGACC AAGGATACAG  
1201 TTGTTCCTC GTGGCGCGC ATGAGTTCGG CCACGCGCTG GGCTTAGATC ATTCCTCAGT  
1261 GCCGGAGGCG CTCATGTACC CTATGTACCG CTTCACTGAG GGGCCCCCT TGCATAAGGA  
1321 CGACGTGAAT GGCATCCGGC ACCTCTATGG TCCTCGCCCT GAACCTGAGC CACGGCCTCC  
1381 AACCACCACC ACACCGCAGC CCACGGCTCC CCCGACGGTC TGCCCCACCG GACCCCCAC  
1441 TGTCCACCCC TCAGAGCGCC CCACAGCTGG CCCCACAGGT CCCCCCTCAG CTGGCCCCAC  
1501 AGGTCCCCC ACTGCTGGCC CTTCTACGGC CACTACTGTG CCTTTGAGTC CGGTGGACGA  
1561 TGCCTGCAAC GTGAACATCT TCGACGCCAT CGCGGAGATT GGAACACAGC TGTATTGTG  
1621 CAAGGATGGG AAGTACTGGC GATTCTCTGA GGGCAGGGG AGCCGGCCGC AGGGCCCTT  
1681 CCTTATCGCC GACAAGTGGC CCGCGCTGCC CCGCAAGCTG GACTCGGTCT TTGAGGAGCC  
1741 GCTCTCCAAG AAGCTTTTCT TCTTCTCTGG GCGCCAGGTG TGGGTGTACA CAGGCGCGTC  
1801 GGTGCTGGC CCGAGGCGTC TGGACAAGCT GGGCCTGGGA GCCGACGTGG CCCAGGTGAC  
1861 CGGGGCCCTC CGGAGTGGCA GGGGAAGAT GCTGCTGTT AGCGGGCGGC GCCTCTGGAG  
1921 GTTCGACGTG AAGGCGCAGA TGGTGGATCC CCGGAGCGCC AGCGAGGTGG ACCGGATGTT  
1981 CCCCGGGGTG CCTTTGGACA CGCACGACGT CTTCCAGTAC CGAGAGAAAG CCTATTCTG  
2041 CCAGGACCGC TTCTACTGGC GCGTGAGTTC CCGGAGTGAG TTGAACCAGG TGGACCAAGT  
2101 GGGCTACGTG ACCTATGACA TCCTGCAGTG CCCTGAGGAC TAGGGCTCCC GTCCTGCTT  
2161 GCAGTGCCAT GTAAATCCCC ACTGGGACCA ACCCTGGGGA AGGAGCCAGT TTGCCGGATA  
2221 CAAACCTGTA TTCTGTTCTG GAGGAAAGGG AGGAGTGGAG GTGGGCTGGG CCCTCTCTC  
2281 TCACCTTGT TTTTGTGG AGTGTCTTA ATAAACTGG ATTCTCTAAC CTTT

Figure 1

## HUMAN OSTEOCLAST-SPECIFIC AND -RELATED GENES

### RELATED APPLICATION

This application is a continuation of application Ser. No. 08/045,270 filed on Apr. 6, 1993 now abandoned.

### BACKGROUND OF THE INVENTION

Excessive bone resorption by osteoclasts contributes to the pathology of many human diseases including arthritis, osteoporosis, periodontitis, and hypercalcemia of malignancy. During resorption, osteoclasts remove both the mineral and organic components of bone (Blair, H. C., et al., *J. Cell Biol.* 102:1164 (1986)). The mineral phase is solubilized by acidification of the sub-osteoclastic lacuna, thus allowing dissolution of hydroxyapatite (Vaes, G., *Clin. Orthop. Relat.* 231:239 (1988)). However, the mechanism(s) by which type I collagen, the major structural protein of bone, is degraded remains controversial. In addition, the regulation of osteoclastic activity is only partly understood. The lack of information concerning osteoclast function is due in part to the fact that these cells are extremely difficult to isolate as pure populations in large numbers. Furthermore, there are no osteoclastic cell lines available. An approach to studying osteoclast function that permits the identification of heretofore unknown osteoclast-specific or -related genes and gene products would allow identification of genes and gene products that are involved in the resorption of bone and in the regulation of osteoclastic activity. Therefore, identification of osteoclast-specific or -related genes or gene products would prove useful in developing therapeutic strategies for the treatment of disorders involving aberrant bone resorption.

### SUMMARY OF THE INVENTION

The present invention relates to isolated DNA sequences encoding all or a portion of osteoclast-specific or -related gene products. The present invention further relates to DNA constructs capable of replicating DNA encoding osteoclast-specific or -related gene products. In another embodiment, the invention relates to a DNA construct capable of directing expression of all or a portion of the osteoclast-specific or -related gene product in a host cell.

Also encompassed by the present invention are prokaryotic or eukaryotic cells transformed or transfected with a DNA construct encoding all or a portion of an osteoclast-specific or -related gene product. According to a particular embodiment, these cells are capable of replicating the DNA construct comprising the DNA encoding the osteoclast-specific or -related gene product, and, optionally, are capable of expressing the osteoclast-specific or -related gene product. Also claimed are antibodies raised against osteoclast-specific or -related gene products, or portions of these gene products.

The present invention further embraces a method of identifying osteoclast-specific or -related DNA sequences and DNA sequences identified in this manner. In one embodiment, cDNA encoding osteoclast is identified as follows: First, human giant cell tumor of the bone was used to 1) construct a cDNA library; 2) produce <sup>32</sup>P-labelled cDNA to use as a stromal cell<sup>+</sup>, osteoclast<sup>+</sup> probe, and 3) produce (by culturing) a stromal cell population lacking osteoclasts. The presence of osteoclasts in the giant cell tumor was confirmed by histological staining for the osteo-

clast marker, type 5 tartrate-resistant acid phosphatase (TRAP) and with the use of monoclonal antibody reagents.

The stromal cell population lacking osteoclasts was produced by dissociating cells of a giant cell tumor, then growing and passaging the cells in tissue culture until the cell population was homogeneous and appeared fibroblastic. The cultured stromal cell population did not contain osteoclasts. The cultured stromal cells were then used to produce a stromal cell<sup>+</sup>, osteoclast<sup>-</sup> <sup>32</sup>P-labelled cDNA probe.

The cDNA library produced from the giant cell tumor of the bone was then screened in duplicate for hybridization to the cDNA probes: one screen was performed with the giant cell tumor cDNA probe (stromal cell<sup>+</sup>, osteoclast<sup>+</sup>), while a duplicate screen was performed using the cultured stromal cell cDNA probe (stromal cell<sup>+</sup>, osteoclast<sup>-</sup>). Hybridization to a stromal<sup>+</sup>, osteoclast<sup>+</sup> probe, accompanied by failure to hybridize to a stromal<sup>+</sup>, osteoclast<sup>-</sup> probe indicated that a clone contained nucleic acid sequences specifically expressed by osteoclasts.

In another embodiment, genomic DNA encoding osteoclast-specific or -related gene products is identified through known hybridization techniques or amplification techniques. In one embodiment, the present invention relates to a method of identifying DNA encoding an osteoclast-specific or -related protein, or gene product, by screening a cDNA library or a genomic DNA library with a DNA probe comprising one or more sequences selected from the group consisting of the DNA sequences set out in Table I (SEQ ID NOs: 1-32). Finally, the present invention relates to an osteoclast-specific or related protein encoded by a nucleotide sequence comprising a DNA sequence selected from the group consisting of the sequences set out in Table I, or their complementary strands.

### BRIEF DESCRIPTION OF FIG. 1

The FIG. 1 shows cDNA sequence (SEQ ID NO: 33) of human gelatinase B, and highlights those portions of the sequence represented by the osteoclast-specific or -related cDNA clones of the present invention.

### DETAILED DESCRIPTION OF THE INVENTION

As described herein, Applicant has identified osteoclast-specific or osteoclast-related nucleic acid sequences. These sequences were identified as follows: Human giant cell tumor of the bone was used to 1) construct a cDNA library; 2) produce <sup>32</sup>P-labelled cDNA to use as a stromal cell<sup>+</sup>, osteoclast<sup>+</sup> probe, and 3) produce (by culturing) a stromal cell population lacking osteoclasts. The presence of osteoclasts in the giant cell tumor was confirmed by histological staining for the osteoclast marker, type 5 acid phosphatase (TRAP). In addition, monoclonal antibody reagents were used to characterize the multinucleated cells in the giant cell tumor, which cells were found to have a phenotype distinct from macrophages and consistent with osteoclasts.

The stromal cell population lacking osteoclasts was produced by dissociating cells of a giant cell tumor, then growing the cells in tissue culture for at least five passages. After five passages the cultured cell population was homogeneous and appeared fibroblastic. The cultured population contained no multinucleated cells at this point, tested negative for type 5 acid phosphatase, and tested variably alkaline phosphatase positive. That is, the cultured stromal cell population did not contain osteoclasts. The cultured stromal

cells were then used to produce a stromal cell<sup>+</sup>, osteoclast<sup>-</sup> <sup>32</sup>P-labelled cDNA probe.

The cDNA library produced from the giant cell tumor of the bone was then screened in duplicate for hybridization to the cDNA probes: one screen was performed with the giant cell tumor cDNA probe (stromal cell<sup>+</sup>, osteoclast<sup>-</sup>), while a duplicate screen was performed using the cultured stromal cell cDNA probe (stromal cell<sup>+</sup> osteoclast<sup>-</sup>). Clones that hybridized to the giant cell tumor cDNA probe (stromal<sup>+</sup>, osteoclast<sup>-</sup>), but not to the stromal cell cDNA probe (stromal<sup>+</sup>, osteoclast<sup>-</sup>), were assumed to contain nucleic acid sequences specifically expressed by osteoclasts.

As a result of the differential screen described herein, DNA specifically expressed in osteoclast cells characterized as described herein was identified. This DNA, and equivalent DNA sequences, is referred to herein as osteoclast-specific or osteoclast-related DNA. Osteoclast-specific or -related DNA of the present invention can be obtained from sources in which it occurs in nature, can be produced recombinantly or synthesized chemically; it can be cDNA, genomic DNA, recombinantly-produced DNA or chemically-produced DNA. An equivalent DNA sequence is one which hybridizes, under standard hybridization conditions, to an osteoclast-specific or -related DNA identified as described herein or to a complement thereof.

Differential screening of a human osteoclastoma cDNA library was performed to identify genes specifically expressed in osteoclasts. Of 12,000 clones screened, 195 clones were identified which are either uniquely expressed in osteoclasts, or are osteoclast-related. These clones were further identified as osteoclast-specific, as evidenced by failure to hybridize to mRNA derived from a variety of unrelated human cell types, including epithelium, fibroblasts, lymphocytes, myelomonocytic cells, osteoblasts, and neuroblastoma cells. Of these, 32 clones contain novel cDNA sequences which were not found in the GenBank database.

A large number of cDNA clones obtained by this procedure were found to represent 92 kDa type IV collagenase (gelatinase B; E.C. 3.4.24.35) as well as tartrate resistant acid phosphatase. In situ hybridization localized mRNA for gelatinase B to multinucleated giant cells in human osteoclastomas. Gelatinase B immunoreactivity was demonstrated in giant cells from 8/8 osteoclastomas, osteoclasts in normal bone, and in osteoclasts of Paget's disease by use of a polyclonal antiserum raised against a synthetic gelatinase B peptide. In contrast, no immunoreactivity for 72 kDa type IV collagenase (gelatinase A; E.C. 3.4.24.24), which is the product of a separate gene, was detected in osteoclastomas or normal osteoclasts.

The present invention has utility for the production and identification of nucleic acid probes useful for identifying osteoclast-specific or -related DNA. Osteoclast-specific or -related DNA of the present invention can be used to produce osteoclast-specific or -related gene products useful in the therapeutic treatment of disorders involving aberrant bone resorption. The osteoclast-specific or -related sequences are also useful for generating peptides which can then be used to produce antibodies useful for identifying osteoclast-specific or -related gene products, or for altering the activity of osteoclast-specific or -related gene products. Such antibodies are referred to as osteoclast-specific antibodies. Osteoclast-specific antibodies are also useful for identifying osteoclasts. Finally, osteoclast-specific or -related DNA sequences of the present invention are useful in gene therapy. For example, they can be used to alter the

expression in osteoclasts of an aberrant osteoclast-specific or -related gene product or to correct aberrant expression of an osteoclast-specific or -related gene product. The sequences described herein can further be used to cause osteoclast-specific or related gene expression in cells in which such expression does not ordinarily occur, i.e., in cells which are not osteoclasts.

#### Example 1—Osteoclast cDNA Library Construction

Messenger RNA (mRNA) obtained from a human osteoclastoma ('giant cell tumor of bone'), was used to construct an osteoclastoma cDNA library. Osteoclastomas are actively bone resorptive tumors, but are usually non-metastatic. In cryostat sections, osteoclastomas consist of ~30% multinucleated cells positive for tartrate resistant acid phosphatase (TRAP), a widely utilized phenotypic marker specific in vivo for osteoclasts (Minkin, *Calcif. Tissue Int.* 34:285-290 (1982)). The remaining cells are uncharacterized 'stromal' cells, a mixture of cell types with fibroblastic/mesenchymal morphology. Although it has not yet been definitively shown, it is generally held that the osteoclasts in these tumors are non-transformed, and are activated to resorb bone in vivo by substance(s) produced by the stromal cell element.

Monoclonal antibody reagents were used to partially characterize the surface phenotype of the multinucleated cells in the giant cell tumors of long bone. In frozen sections, all multinucleated cells expressed CD68, which has previously been reported to define an antigen specific for both osteoclasts and macrophages (Horton, M. A. and M. H. Helfrich, In *Biology and Physiology of the Osteoclast*, B. R. Rifkin and C. V. Gay, editors, CRC Press, Inc. Boca Raton, Fla., 33-54 (1992)). In contrast, no staining of giant cells was observed for CD11b or CD14 surface antigens, which are present on monocyte/macrophages and granulocytes (Arnaout, M. A. et al. *J. Cell. Physiol.* 137:305 (1988); Haziot, A. et al. *J. Immunol.* 141:547 (1988)). Cytocentrifuge preparations of human peripheral blood monocytes were positive for CD68, CD11b, and CD14. These results demonstrate that the multinucleated giant cells of osteoclastomas have a phenotype which is distinct from that of macrophages, and which is consistent with that of osteoclasts.

Osteoclastoma tissue was snap frozen in liquid nitrogen and used to prepare poly A<sup>+</sup> mRNA according to standard methods. cDNA cloning into a pcDNAII vector was carried out using a commercially-available kit (Librarian, In Vitrogen). Approximately 2.6×10<sup>6</sup> clones were obtained, >95% of which contained inserts of an average length 0.6 kB.

#### Example 2—Stromal Cell mRNA Preparation

A portion of each osteoclastoma was snap frozen in liquid nitrogen for mRNA preparation. The remainder of the tumor was dissociated using brief trypsinization and mechanical disaggregation, and placed into tissue culture. These cells were expanded in Dulbecco's MEM (high glucose, Sigma) supplemented with 10% newborn calf serum (MA Bioproducts), gentamycin (0.5 mg/ml), l-glutamine (2 mM) and non-essential amino acids (0.1 mM) (Gibco). The stromal cell population was passaged at least five times, after which it showed a homogenous, fibroblastic looking cell population that contained no multinucleated cells. The stromal cells were mononuclear, tested negative acid phosphatase, and tested variably alkaline phosphatase positive. These findings indicate that propagated stromal cells (i.e., stromal cells that

are passaged in culture) are non-osteoclastic and non-activated.

**Example 3—Identification of DNA Encoding Osteoclastoma-Specific or -Related Gene Products by Differential Screening of an Osteoclastoma cDNA Library**

A total of 12,000 clones drawn from the osteoclastoma cDNA library were screened by differential hybridization, using mixed <sup>32</sup>P labelled cDNA probes derived from (1) giant cell tumor mRNA (stromal cell<sup>+</sup>, OC<sup>+</sup>), and (2) mRNA from stromal cells (stromal cell<sup>+</sup>, OC<sup>-</sup>) cultivated from the same tumor. The probes were labelled with <sup>32</sup>PdCTP by random priming to an activity of ~10<sup>6</sup>CPM/μg. Of these 12,000 clones, 195 gave a positive hybridization signal with giant cell (i.e., osteoclast and stromal cell) mRNA, but not with stromal cell mRNA. Additionally, these clones failed to hybridize to cDNA produced from mRNA derived from a variety of unrelated human cell types including epithelial cells, fibroblasts, lymphocytes, myelomonocytic cells, osteoblasts, and neuroblastoma cells. The failure of these clones to hybridize to cDNA produced from mRNA derived from other cell types supports the conclusion that these clones are either uniquely expressed in osteoclasts, or are osteoclast-related.

The osteoclast (OC) cDNA library was screened for differential hybridization to OC cDNA (stromal cell<sup>+</sup>, OC<sup>+</sup>) and stromal cell cDNA (stromal cell<sup>+</sup>, OC<sup>-</sup>) as follows:

NYTRAN filters (Schleicher & Schuell) were placed on agar plates containing growth medium and ampicillin. Individual bacterial colonies from the OC library were randomly picked and transferred, in triplicate, onto filters with pre-ruled grids and then onto a master agar plate. Up to 200 colonies were inoculated onto a single 90-mm filter/plate using these techniques. The plates were inverted and incubated at 37° C. until the bacterial inoculates had grown (on the filter) to a diameter of 0.5–1.0 mm.

The colonies were then lysed, and the DNA bound to the filters by first placing the filters on top of two pieces of Whatman 3 MM paper saturated with 0.5N NaOH for 5 minutes. The filters were neutralized by placing on two pieces of Whatman 3 MM paper saturated with 1M Tris-HCl, pH 8.0 for 3–5 minutes. Neutralization was followed by incubation on another set of Whatman 3 MM papers saturated with 1M Tris-HCl, pH 8.0/1.5M NaCl for 3–5 minutes. The filters were then washed briefly in 2×SSC.

DNA was immobilized on the filters by baking the filters at 80° C. for 30 minutes. Filters were best used immediately, but they could be stored for up to one week in a vacuum jar at room temperature.

Filters were prehybridized in 5–8 ml of hybridization solution per filter, for 2–4 hours in a heat sealable bag. An additional 2 ml of solution was added for each additional filter added to the hybridization bag. The hybridization

buffer consisted of 5×SSC, 5×Denhardt's solution, 1% SDS and 100 μg/ml denatured heterologous DNA.

Prior to hybridization, labeled probe was denatured by heating in 1×SSC for 5 minutes at 100° C., then immediately chilled on ice. Denatured probe was added to the filters in hybridization solution, and the filters hybridized with continuous agitation for 12–20 hours at 65° C.

After hybridization, the filters were washed in 2×SSC/0.2% SDS at 50°–60° C. for 30 minutes, followed by washing in 0.2×SSC/0.2% SDS at 60° C. for 60 minutes.

The filters were then air dried and autoradiographed using an intensifying screen at -70° C. overnight.

**Example 4—DNA Sequencing of Selected Clones**

Clones reactive with the mixed tumor probe, but unreactive with the stromal cell probe, are expected to contain either osteoclast-related, or in vivo 'activated' stromal-cell-related gene products. One hundred and forty-four cDNA clones that hybridized to tumor cell cDNA, but not to stromal cell cDNA, were sequenced by the dideoxy chain termination method of Sanger et al. (Sanger F., et al. *Proc. Natl. Acad. Sci. USA* 74:5463 (1977)) using sequenase (US Biochemical). The DNASIS (Hitachi) program was used to carry out sequence analysis and a homology search in the GenBank/EMBL database.

Fourteen of the 195 tumor<sup>+</sup> stromal<sup>-</sup> clones were identified as containing inserts with a sequence identical to the osteoclast marker, type 5 tartrate-resistant acid phosphatase (TRAP) (GenBank accession number J04430 M19534). The high representation of TRAP positive clones also indicates the effectiveness of the screening procedure in enriching for clones which contain osteoclast-specific or related cDNA sequences.

Interestingly, an even larger proportion of the tumor<sup>+</sup> stromal<sup>-</sup> clones (77/195; 39.5%) were identified as human gelatinase B (macrophage-derived gelatinase) (Wilhelm, S. M. *J. Biol. Chem.* 264:17213 (1989)), again indicating high expression of this enzyme by osteoclasts. Twenty-five of the gelatinase B clones were identified by dideoxy sequence analysis; all 25 showed 100% sequence homology to the published gelatinase B sequence (Genbank accession number J05070). The portions of the gelatinase B cDNA sequence covered by these clones is shown in the FIGURE (SEQ ID NO: 33). An additional 52 gelatinase B clones were identified by reactivity with a <sup>32</sup>P-labelled probe for gelatinase B.

Thirteen of the sequenced clones yielded no readable sequence. A DNASIS search of GenBank/EMBL databases revealed that, of the remaining 91 clones, 32 clones contain novel sequences which have not yet been reported in the databases or in the literature. These partial sequences are presented in Table I. Note that three of these sequences were repeats, indicating fairly frequent representation of mRNA related to this sequence. The repeat sequences are indicated by <sup>a</sup>, <sup>b</sup> superscripts (Clones 198B, 223B and 32C of Table I).

TABLE I

PARTIAL SEQUENCES OF 32 NOVEL OC-SPECIFIC OR -RELATED EXPRESSED GENES (cDNA CLONES)

34A (SEQ ID NO: 1)					
1 GCAAATATCT	AAGTTTATTG	CTTGGATTTC	TAGTGAGAGC	TGTTGAATTT	GGTGATGTCA
61 AATGTTTCTA	GGGTTTTTTT	AGTTTGTTTT	TATTGAAAAA	TTTAATTAT	TATGCTATAG
121 GTGATATCT	CITTTGAATAA	ACCTATAATA	GAAATATGCA	GCAGACAACA	
4B (SEQ ID NO: 2)					
1 GTGTCAACCT	GCATATCTTA	AAAATGTCAA	AATGCTGCAT	CTGTTAATG	TCGGGGTAGG

TABLE I-continued

PARTIAL SEQUENCES OF 32 NOVEL OC-SPECIFIC OR -RELATED  
EXPRESSED GENES (cDNA CLONES)

61 GGG					
12B (SEQ ID NO: 3)					
1 CTTCCTCTC	TTGCTTCCCT	TTCCCAAGCA	GAGGTGCTCA	CTCCATGGCC	ACCGCCACCA
61 CAGGCCACACA	GGGAGTACTG	CCAGACTACT	GCTGATGTTT	TCCTAAGGCC	CAGGGAGTCT
121 CAACAGCTG	GTGGTGAATG	CTGCTGGCA	CGGGACCCCC	CCC	
28B (SEQ ID NO: 4)					
1 TTTTATTGT	AAATATATGT	ATTACATCCC	TAGAAAAAGA	ATCCCAGGAT	TTTCCCTCCT
61 GTGTGTTTTC	GTCTTGCTTC	TTCATGGTCC	ATGATGCCAG	CTGAGGTTGT	CAGTACAATG
121 AAACCAAACT	GCGGGGATGG	AAGCAGATTA	TTCTGCCATT	TTTCCAGGTC	TTT
37B (SEQ ID NO: 5)					
1 GGCTGGACAT	GGGTGCCCTC	CACGTCCCTC	ATATCCCCAG	GCACACTCTG	GCCTCAGGTT
61 TTGCCCTGGC	CATGTCATCT	ACCTGGAGTG	GGCCCTCCCCC	TTCTTCAGCC	TTGAATCAAA
121 AGCCACTTTG	TTAGGCGAGG	ATTTCACAGA	CCACTCATCA	CATTAAAAAA	TATTTTGAAG
181 ACAAAAAAAA	AAAAAAA				
55B (SEQ ID NO: 6)					
1 TTGACAAAGC	TGTTTATTTT	CACCAATAAA	TAGTATATGG	TGATTGGGGT	TTCTATTTAT
61 AAGAGTAGTG	GCTATTATAT	GGGGTATCAT	GTTGATGCTC	ATAAATAGTT	CATACTACT
121 TAAATTCCT	TC				
60B (SEQ ID NO: 7)					
1 GAAGAGAGTT	GTATGTACAA	CCCCAACAGG	CAAGGCAGCT	AAATGCAGAG	GGTACAGAGA
61 GATCCCGAGG	GAATT				
86B (SEQ ID NO: 8)					
1 GGATGGAAAC	ATGTAGAAAT	CCAGAGAAAA	ACAAATTTAA	AAAAAGGTGG	AAAAGTTACG
61 GCAAACTCTGA	GATTTTCAGCA	TAAATCTTT	AGTTAGAAAT	GAGAGAAAAA	AGAGGGAGGC
121 TGGTTGCTGT	TGCACGTATC	AATAGGTTAT	C		
87B (SEQ ID NO: 9)					
1 TTCTTGATCT	TTAGAACACT	ATGAATAGGG	AAAAAGAAA	AAACTGTTCA	AAATAAAATG
61 TAGGAGCCGT	GCTTTTGGAA	TGCTTGAGTG	AGGAGCTCAA	CAAGTCCTCT	CCCAAGAAAG
181 CAATGATAAA	ACTTGACAAA	A			
98B (SEQ ID NO: 10)					
1 ACCCATTTCT	AACAATTTT	ACTGTAAAAT	TTTTGGTCAA	AGTTCTAAGC	TTAATCACAT
61 CTCAAAGAAAT	AGAGGCAATA	TATAGCCCAT	CTTACTAGAC	ATACAGTATT	AAACTGGACT
121 GAATATGAGG	ACAAGCTCTA	GTGGTCATTA	AAACCCCTCAG	AA	
110B (SEQ ID NO: 11)					
1 ACATATATTA	ACAGCATTTCA	TTTGGCCAAA	ATCTACACGT	TTGTAGAATC	CTACTGTATA
61 TAAAGTGGGA	ATGTATCAAG	TATAGACTAT	GAAAGTGCAA	ATAACAAGTC	AAGGTTAGAT
121 TAACCTTTTT	TTTTTACATT	ATAAAATTAA	CTTGT		
118B (SEQ ID NO: 12)					
1 CCAAATTTCT	CTGGAATCCA	TCCTCCCTCC	CATCACCATA	GCCTCGAGAC	GTCATTTCTG
61 TTTGACTACT	CCAGC				
133B (SEQ ID NO: 13)					
1 AACTAACCTC	CTCGGACCCC	TGCTCACTC	ATTTACACCA	ACCACCCAAC	TATCTATAAA
61 CCTGAGCCAT	GGCCATCCCT	TATGAGCGGC	GCAGTGATTA	TAGGCTTTCC	CTCTAAGATA
121 AAAT					
140B (SEQ ID NO: 14)					
1 ATTATTATTC	TTTTTTTATG	TTAGCTTAGC	CATGCAAAAT	TTACTGGTGA	AGCAGTTAAT
61 AAAACACACA	TCCCATTGAA	GGGTTTGTGA	CATTTCAGTC	CTTACAAATA	ACAAAGCAAT
121 GATAAACCCG	GCACGTCCTG	GCAGGAAATT	C		
144B (SEQ ID NO: 15)					
1 CGTGACACAA	ACATGCATT	GTTTTATTCA	TAAACAGCC	TGGTTTCTTA	AAACAATACA
61 AACAGCATGT	TCATCAGCAG	GAAGCTGGCC	GTGGGCAGGG	GGGCC	
198B (SEQ ID NO: 16)					
1 ATAGGTIAGA	TTCTCATTCA	CGGGACTAGT	TAGCTTTAAG	CACCCCTAGAG	GACTAGGGTA
61 ATCTGACTTC	TCACTTCCTA	AGTTCCTCT	TATATCTCA	AGGTAGAAAT	GTCTATGTTT
121 TCTACTCCAA	TTCAATAATC	TATTCATAAG	TCITTTGGTAC	AAGTTACATG	ATAAAAAAGAA
181 ATGTGATTG	TCITCCCTTC	TTTGACATTT	TRAATAAAG	TATTTATCTC	CTGTCTACAG
241 TTTAAT					
212B (SEQ ID NO: 17)					
1 GTCCAGTATA	AAGGAAAGCG	TTAAGTCGGT	AAGCTAGAGG	ATGTAAATA	TCTTTTATGT
61 CCTCTAGATA	AAACACCCGA	TTAACAGATG	TTAACCTTTT	ATGTTTGTAT	TTGCTTTAAA
121 AATGGCCCTC	TACACATTAG	CTCCAGCTAA	AAAGACACAT	TGAGAGCTTA	GAGGATAGTC
181 TCTGGAGC					
223B (SEQ ID NO: 18)					
1 GCACTTGGAA	GGGAGTTGGT	GTGCTATTTT	TGAAGCAGAT	GTGGTGATAC	TGAGATTGTC
61 TGTTCACTTT	CCCCATTTGT	TTGTGCTTCA	AATGATCCTT	CCTACTTTGC	TTCTCTCCAC
121 CCATGACCTT	TTTCACTGTG	GCCATCAAGG	ACTTCTCTGA	CAGCTTGTGT	ACTCTTAGGC
181 TAAGAGATGT	GACTACAGCC	TGCCCTGAC	TG		
241B (SEQ ID NO: 19)					
1 TGTTAGTTTT	TAGGAAGGCC	TGTCCTCTGG	GAGTGAGGTT	TATTAGTCCA	CTTCTTGGAG
61 CTAGACGTCC	TATAGTTAGT	CACCTGGGGAT	GGTGAAAGAG	GGAGAAAGAGG	AAGGGCGAAG
121 GGAAGGGCTC	TTTGCTAGTA	TCTCCAATTC	TAGAAGATGG	TTTAGATGAT	AACCACAGGT
181 CTATATGAGC	ATAGTAAGGC	TGT			
32C (SEQ ID NO: 20)					
1 CCTATTCTG	ATCTGACTT	TGGACAAGGC	CCTTCAGCCA	GAAGACTGAC	AAAGTCATCC
121 TCCGTCTACC	AGAGCGTGCA	CTGTGATCC	TAAATAAAGC	TTCTCTCCG	GCTGTGCCCT
161 GGGTGGAAGG	GGCAGGATTC	TGCAGCTGCT	TTTGCAATTC	TCTTCTAAA	TTTCAIT

TABLE I-continued

PARTIAL SEQUENCES OF 32 NOVEL OC-SPECIFIC OR -RELATED EXPRESSED GENES (cDNA CLONES)					
34C (SEQ ID NO: 21)	GTGTGTTTAT	TCCTGTACAA	ATCATTACAA	AACCAAGTCT	GGGGCAGTCA
1 CGGAGGOTAG	CCATCACCCC	AGTGCAATGG	CTAGCTGCTG	GOCITT	
61 CCGCCCCCAC					
47C (SEQ ID NO: 22)	CAAAGCAGGC	AACCCCTTT	GGCACTGCTG	CCACTGGGGT	CATGGCGGTT
1 TTAGTTCACT	GGGAGGTTTC	COCAACACCC	TOCTCTGCTT	CCCTGTGTGT	CGGGGTCTCA
61 GTGGCAGCTG	CAGAGTGGG				
121 GGAGCTGACC					
65C (SEQ ID NO: 23)	TAAAGAGAT	TTTGGTCTTA	AAGGCTTCAT	CATGAAAGTG	TACATGCATA
1 GCTGAATGTT	AATTACGTGG	TATGGATGGT	TGCTTGTTTA	TAACTAAAG	ATGTACAGCA
61 TGCAAGTGTG	TTAGAGTCTT	CTAATATTG	ATGTCTTAAC	ACTGGGTCTG	CTTATGC
121 AACTGCCCT					
79C (SEQ ID NO: 24)	TATGGAATCC	AGAAGGGAAA	CAAGCACTGG	ATAATTAAAA	ACAGCTGGGG
1 GGCAGTGGGA	GGAAACAAAG	GATATATCT	CATGGCTCGA	AATAAGAACA	ACGCTGTGG
61 AGAAACTGG	CTGGCCAGCT	TCCCAAGAT	GTGACTCCAG	CCAGAAA	
121 CATTGCCAAC					
84C (SEQ ID NO: 25)	ACCGTCTTTA	TTCTCTCTCT	GCCTCAGAGG	TCAGGAAGGA	GGTCTGGCAG
1 GCCAGGGCGG	GGGCGCTAGT	CATCTGTGGC	AGCGAAGGTG	AAGGGACTCA	CCTTGTGGCC
61 GACCTGCACT	TAGAATTGT	TCTGGAATTC	C		
121 CGTGGCTGAG					
86C (SEQ ID NO: 26)	CACTCTGGTA	TTTTTAGTTT	AACAATATAT	GTGTTGTGTC	TTGGAAAITA
1 AACTCTTTCA	ATTCTATTTG	AGCTGTCTCA	TTCTTTTTTT	AATGGTCATA	TACAGTAGTA
61 GTTCATATCA	AGAATATATC	CTAATACTTT	TTAAAA		
121 TTCAATTATA					
87C (SEQ ID NO: 27)	GAAGGCCTGA	GGCCTAGGGG	CCGRGGCTGG	CCTGCGTCTC	AGTCTGGGGA
1 GGATAAGAAA	CGCACAGGTT	GAGAGGGGCA	CTTCTCTTGG	CTTAGGTTGG	TGAGGATCTG
61 CGCAGCAGCC	GCCGGTGGAG	AGCCACAAA			
121 GTCCTGGTTG					
88C (SEQ ID NO: 28)	AGAGTTTGAC	CTGGAGCCGG	ATACCTACTG	CCGCTATGAC	TCGGTCAGCG
1 CTGACCTTCG	AGCGGTGAGC	GACGACTCCG	GTGGGGAAGT	TCTGCGGCGA	T
61 TGTTCAACGG					
89C (SEQ ID NO: 29)	GTGGATAGTG	CTTTTGTTGA	GCAAATGCTC	CCTCCTTAAG	GTTATAGGGC
1 ATCCCTGGCT	TGGGAGTGTG	GAAGTACTAC	TTAAGTGTCT	GTOCTGCTTG	GCTGTGTTA
61 TCCCTGAGTT	GTGATGTTGT	GCTAACATA	AGAATAC		
121 TCGTTTTCTG					
101C (SEQ ID NO: 30)	CCCTCTCTCT	CTCCATCCCC	ATACATCACC	AGGTCTAATG	TTTACAAACG
1 GGCTGGGCAT	CCGCTCTGAAO	CCAAGGGCCG	TCCGTGCCAC	GGTGCTGTG	AGTATTCTCT
61 GTGCCAGCCC	CCCATAAGGT	TGGAGTATCT	GC		
121 CGTTAGCTTT					
112C (SEQ ID NO: 31)	COGCGATACA	GACCCACAGA	GTGCCATCCC	TGAGAGACCA	GACCGCTCCC
1 CCAACTCCTA	CTAAAATAAA	CATGAAGCAC			
161 CAATACTCTC					
114C (SEQ ID NO: 32)	TGTCTCATGG	TGGGAAGGAA	CATGGTACAT	TTC	
1 CATGGATGAA					

\*Repeated 3 times

\*Repeated 2 times

Sequence analysis of the OC<sup>+</sup> stromal cell<sup>+</sup> cloned DNA sequences revealed, in addition to the novel sequences, a number of previously-described genes. The known genes identified (including type 5 acid phosphatase, gelatinase B, cystatin C (13 clones), Alu repeat sequences (11 clones), creatine kinase (6 clones) and others) are summarized in Table II. In situ hybridization (described below) directly demonstrated that gelatinase B mRNA is expressed in multinucleated osteoclasts and not in stromal cells. Although gelatinase B is a well-characterized protease, its expression at high levels in osteoclasts has not been previously described. The expression in osteoclasts of cystatin C, a cysteine protease inhibitor, is also unexpected. This finding has not yet been confirmed by in situ hybridization. Taken together, these results demonstrate that most of these identified genes are osteoclast-expressed, thereby confirming the effectiveness of the differential screening strategy for identifying DNA encoding osteoclast-specific or -related gene products. Therefore, novel genes identified by this method have a high probability of being OC-specific or related.

In addition, a minority of the genes identified by this screen are probably not expressed by OCs (Table II). For example, type III collagen (6 clones), collagen type I (1 clone), dermatansulfate (1 clone), and type VI collagen (1

clone) are more likely to originate from the stromal cells or from osteoblastic cells which are present in the tumor. These cDNA sequences survive the differential screening process either because the cells which produce them in the tumor in vivo die out during the stromal cell propagation phase, or because they stop producing their product in vitro. These clones do not constitute more than 5-10% of the all sequences selected by differential hybridization.

TABLE II

SEQUENCE ANALYSIS OF CLONES ENCODING KNOWN SEQUENCES FROM AN OSTEOCLASTOMA cDNA LIBRARY	
Clones with Sequence Homology to Collagenase Type IV	25 total
Clones with Sequence Homology to Type 5 Tartrate Resistant Acid Phosphatase	14 total
Clones with Sequence Homology to Cystatin C:	13 total
Clones with Sequence Homology to Alu-repeat Sequences	11 total
Clones with Sequence Homology to Creatine Kinase	6 total
Clones with Sequence Homology to	6 total

TABLE II-continued

SEQUENCE ANALYSIS OF CLONES ENCODING KNOWN SEQUENCES FROM AN OSTEOCLASTOMA cDNA LIBRARY	
Type III Collagen	5 total
Clones with Sequence Homology to MHC Class I $\gamma$ Invariant Chain	3 total
Clones with Sequence Homology to MHC Class II $\beta$ Chain	10 total
One or Two Clone(s) with Sequence Homology to Each of the Following:	
$\alpha 1$ collagen type I	
$\gamma$ interferon inducible protein	
osteopontin	
Human chondroitin/dermatan sulfate	
$\alpha$ globin	
$\beta$ glucosidase/sphingolipid activator	
Human CAPL protein (Ca binding)	
Human EST 01024	
Type VI collagen	
Human EST 00553	

#### Example 5—In situ Hybridization of OC-Expressed Genes

In situ hybridization was performed using probes derived from novel cloned sequences in order to determine whether the novel putative OC-specific or -related genes are differentially expressed in osteoclasts (and not expressed in the stromal cells) of human giant cell tumors. Initially, in situ hybridization was performed using antisense (positive) and sense (negative control) cRNA probes against human type IV collagenase/gelatinase B labelled with  $^{35}$ S-UTP.

A thin section of human giant cell tumor reacted with the antisense probe resulted in intense labelling of all OCs, as indicated by the deposition of silver grains over these cells, but failed to label the stromal cell elements. In contrast, only minimal background labelling was observed with the sense (negative control) probe. This result confirmed that gelatinase B is expressed in human OCs.

In situ hybridization was then carried out using cRNA probes derived from 11/32 novel genes, labelled with digoxigenin UTP according to known methods.

The results of this analysis are summarized in Table III. Clones 28B, 118B, 140B, 198B, and 212B all gave positive reactions with OCs in frozen sections of a giant cell tumor, as did the positive control gelatinase B. These novel clones therefore are expressed in OCs and fulfill all criteria for OC-relatedness. 198B is repeated three times, indicating relatively high expression. Clones 4B, 37B, 88C and 98B produced positive reactions with the tumor tissue; however the signal was not well-localized to OCs. These clones are therefore not likely to be useful and are eliminated from further consideration. Clones 86B and 87B failed to give a positive reaction with any cell type, possibly indicating very low level expression. This group of clones could still be useful but may be difficult to study further. The results of this analysis show that 5/11 novel genes are expressed in OCs, indicating that ~50% of novel sequences likely to be OC-related.

To generate probes for the in situ hybridizations, cDNA derived from novel cloned osteoclast-specific or -related cDNA was subcloned into a BlueScript II SK(-) vector. The orientation of cloned inserts was determined by restriction analysis of subclones. The T7 and T3 promoters in the BlueScriptII vector was used to generate  $^{35}$ S-labelled ( $^{35}$ S-UTP 850 Ci/mmol, Amersham, Arlington Heights, Ill.), or

UTP digoxigenin labelled cRNA probes.

TABLE III

In Situ HYBRIDIZATION USING PROBES DERIVED FROM NOVEL SEQUENCES			
Clone	Reactivity with:		
	Osteoclasts	Stromal Cells	
4B	+	+	10
28B*	+	-	
37B	+	+	
86B	-	-	
87B	-	-	
88C	+	+	15
98B	+	+	
118B*	+	-	
140B*	+	-	
198B*	+	-	
212B*	+	-	20
Gelatinase B*	+	-	

\*OC-expressed, as indicated by reactivity with antisense probe and lack of reactivity with sense probe on OCs only.

In situ hybridization was carried out on 7 micron cryostat sections of a human osteoclastoma as described previously (Chang, L.-C. et al. *Cancer Res.* 49:6700 (1989)). Briefly, tissue was fixed in 4% paraformaldehyde and embedded in OCT (Miles Inc., Kankakee, Ill.). The sections were rehydrated, postfixed in 4% paraformaldehyde, washed, and pretreated with 10 mM DTT, 10 mM iodoacetamide, 10 mM N-ethylmaleimide and 0.1 triethanolamine-HCL. Prehybridization was done with 50% deionized formamide, 10 mM Tris-HCl, pH 7.0, 1x Denhardt's, 500 mg/ml tRNA, 80 mg/ml salmon sperm DNA, 0.3M NaCl, mM EDTA, and 100 mM DTT at 45° C. for 2 hours. Fresh hybridization solution containing 10% dextran sulfate and 1.5 ng/ml  $^{35}$ S-labelled or digoxigenin labelled RNA probe was applied after heat denaturation. Sections were coverslipped and then incubated in a moistened chamber at 45°-50° C. overnight. Hybridized sections were washed four times with 50% formamide, 2x SSC, containing 10 mM DTT and 0.5% Triton X-100 at 45° C. Sections were treated with RNase A and RNase T1 to digest single-stranded RNA, washed four times in 2x SSC/10 mM DTT.

In order to detect  $^{35}$ S-labelling by autoradiography, slides were dehydrated, dried, and coated with Kodak NTB-2 emulsion. The duplicate slides were split, and each set was placed in a black box with desiccant, sealed, and incubated at 4° C. for 2 days. The slides were developed (4 minutes) and fixed (5 minutes) using Kodak developer D19 and Kodak fixer. Hematoxylin and eosin were used as counterstains.

In order to detect digoxigenin-labelled probes, a Nucleic Acid Detection Kit (Boehringer-Mannheim, Cat. #1175041) was used. Slides were washed in Buffer 1 consisting of 100 mM Tris/150 mM NaCl, pH7.5, for 1 minute. 100  $\mu$ l Buffer 2 was added (made by adding 2 mg/ml blocking reagent as provided by the manufacturer) in Buffer 1 to each slide. The slides were placed on a shaker and gently swirled at 20° C.

Antibody solutions were diluted 1:100 with Buffer 2 (as provided by the manufacturer). 100  $\mu$ l of diluted antibody solution was applied to the slides and the slides were then incubated in a chamber for 1 hour at room temperature. The slides were monitored to avoid drying. After incubation with antibody solution, slides were washed in Buffer 1 for 10 minutes, then washed in Buffer 3 containing 2 mM levamisole for 2 minutes.

After washing, 100  $\mu$ l color solution was added to the slides. Color solution consisted of nitroblue/tetrazolium salt



(NBT) (1:225 dilution) 4.5  $\mu$ l, 5-bromo-4-chloro-3-indolyl phosphate (1:285 dilution) 3.5  $\mu$ l, levamisole 0.2 mg in Buffer 3 (as provided by the manufacturer) in a total volume of 1 ml. Color solution was prepared immediately before use.

After adding the color solution, the slides were placed in a dark, humidified chamber at 20° C. for 2-5 hours and monitored for color development. The color reaction was stopped by rinsing slides in TE Buffer.

The slides were stained for 60 seconds in 0.25% methyl green, washed with tap water, then mounted with water-based Permount (Fisher).

#### Example 6—Immunohistochemistry

Immunohistochemical staining was performed on frozen and paraffin embedded tissues as well as on cytospin preparations (see Table IV). The following antibodies were used: polyclonal rabbit anti-human gelatinase antibodies; Ab110 for gelatinase B; monoclonal mouse anti-human CD68 antibody (clone KP1) (DAKO, Denmark); Mo1 (anti-CD11b) and Mo2 (anti-CD14) derived from ATCC cell lines HB CRL 8026 and TIB 228/HB44. The anti-human gelatinase B antibody Ab110 was raised against a synthetic peptide with the amino acid sequence EALMYPMYRFTEGPPLHK (SEQ ID NO: 34), which is specific for human gelatinase B (Corcoran, M. L. et al. *J. Biol. Chem.* 267:515 (1992)).

Detection of the immunohistochemical staining was achieved by using a goat anti-rabbit glucose oxidase kit (Vector Laboratories, Burlingame Calif.) according to the manufacturer's directions. Briefly, the sections were rehydrated and pretested with either acetone or 0.1% trypsin. Normal goat serum was used to block nonspecific binding. Incubation with the primary antibody for 2 hours or overnight (Ab110:1/500 dilution) was followed by either a glucose oxidase labeled secondary anti-rabbit serum, or, in the case of the mouse monoclonal antibodies, were reacted with purified rabbit anti-mouse Ig before incubation with the secondary antibody.

Paraffin embedded and frozen sections from osteoclastomas (GCT) were reacted with a rabbit antiserum against gelatinase B (antibody 110) (Corcoran, M. L. et al. *J. Biol. Chem.* 267:515 (1992)), followed by color development with glucose oxidase linked reagents. The osteoclasts of a giant cell tumor were uniformly strongly positive for gelatinase B, whereas the stromal cells were unreactive. Control sections reacted with rabbit preimmune serum were negative. Identical findings were obtained for all 8 long bone giant cell tumors tested (Table IV). The osteoclasts present in three out of four central giant cell granulomas (CGG) of the mandible were also positive for gelatinase B expression. These neoplasms are similar but not identical to the long bone giant cell tumors, apart from their location in the jaws (Shafer, W. G. et al., *Textbook of Oral Pathology*, W. B. Saunders Company, Philadelphia, pp. 144-149 (1983)). In contrast, the multinucleated cells from a peripheral giant cell tumor, which is a generally non-resorptive tumor of oral soft tissue,

were unreactive with antibody (Shafer, W. G. et al., *Textbook of Oral Pathology*, W. B. Saunders Company, Philadelphia, pp. 144-149 (1983)).

Antibody 110 was also utilized to assess the presence of gelatinase B in normal bone (n=3) and in Paget's disease, in which there is elevated bone remodeling and increased osteoclastic activity. Strong staining for gelatinase B was observed in osteoclasts both in normal bone (mandible of a 2 year old), and in Paget's disease. Staining was again absent in controls incubated with preimmune serum. Osteoblasts did not stain in any of the tissue sections, indicating that gelatinase B expression is limited to osteoclasts in bone. Finally, peripheral blood monocytes were also reactive with antibody 110 (Table IV).

TABLE IV

DISTRIBUTION OF GELATINASE B IN VARIOUS TISSUES

Samples	Antibodies tested Ab 110 gelatinase B
GCT frozen (n = 2)	
giant cells	+
stromal cells	-
GCT paraffin (n = 6)	
giant cells	+
stromal cells	-
central GCG (n = 4)	
giant cells	+(%)
stromal cells	-
peripheral GCT (n = 4)	
giant cells	-
stromal cells	-
Paget's disease (n = 1)	
osteoclasts	+
osteoblasts	-
normal bone (n = 3)	
osteoclasts	+
osteoblasts	-
monocytes (cytospin)	+

Distribution of gelatinase B in multinucleated giant cells, osteoclasts, osteoblasts and stromal cells in various tissues. In general, paraffin embedded tissues were used for these experiments; exceptions are indicated.

#### Equivalents

Those skilled in the art will recognize, or be able to ascertain using no more than routine experimentation, many equivalents to the specific embodiments described herein. Such equivalents are intended to be encompassed by the following claims.

#### SEQUENCE LISTING

(1) GENERAL INFORMATION:

(111) NUMBER OF SEQUENCES: 34

-continued

## ( 2 ) INFORMATION FOR SEQ ID NO:1:

- ( i ) SEQUENCE CHARACTERISTICS:  
 ( A ) LENGTH: 170 base pairs  
 ( B ) TYPE: nucleic acid  
 ( C ) STRANDEDNESS: double  
 ( D ) TOPOLOGY: linear

( i i ) MOLECULE TYPE: DNA (genomic)

( x i ) SEQUENCE DESCRIPTION: SEQ ID NO:1:

```
GCAAAATATCT AAGTTTATTG CTTGATTTT TAGTGAGAGC TGTGAATTT GGTGATGTCA      60
AATGTTTCTA GGGTTTTTTT AGTTTGTTT TATTGAAAAA TTTAATTATT TATGCTATAG      120
GTGATATTCT CTTTGAATAA ACCTATAATA GAAAATAGCA GCAGACAACA      170
```

## ( 2 ) INFORMATION FOR SEQ ID NO:2:

- ( i ) SEQUENCE CHARACTERISTICS:  
 ( A ) LENGTH: 63 base pairs  
 ( B ) TYPE: nucleic acid  
 ( C ) STRANDEDNESS: double  
 ( D ) TOPOLOGY: linear

( i i ) MOLECULE TYPE: DNA (genomic)

( x i ) SEQUENCE DESCRIPTION: SEQ ID NO:2:

```
GTGTCAACCT GCATATCCTA AAAATOTCAA AATGCTGCAT CTGTTAATG TCGGGGTAGG      60
GGG                                                                63
```

## ( 2 ) INFORMATION FOR SEQ ID NO:3:

- ( i ) SEQUENCE CHARACTERISTICS:  
 ( A ) LENGTH: 163 base pairs  
 ( B ) TYPE: nucleic acid  
 ( C ) STRANDEDNESS: double  
 ( D ) TOPOLOGY: linear

( i i ) MOLECULE TYPE: DNA (genomic)

( x i ) SEQUENCE DESCRIPTION: SEQ ID NO:3:

```
CTTCCCTCTC TTGCTTCCTT TTCCCAAGCA GAGGTGCTCA CTCCATGCCC ACCGCCACCA      60
CAGGCCACCA GGAAGTACTG CCAGACTACT GCTGATGTTT TCTTAAGGCC CAAGGAGTCT      120
CAACCAAGCTG GTGGTGAATG CTGCCTGGCA CGGGACCCCC CCC                      163
```

## ( 2 ) INFORMATION FOR SEQ ID NO:4:

- ( i ) SEQUENCE CHARACTERISTICS:  
 ( A ) LENGTH: 173 base pairs  
 ( B ) TYPE: nucleic acid  
 ( C ) STRANDEDNESS: double  
 ( D ) TOPOLOGY: linear

( i i ) MOLECULE TYPE: DNA (genomic)

( x i ) SEQUENCE DESCRIPTION: SEQ ID NO:4:

```
TTTTATTTGT AAATATATGT ATTACATCCC TAGAAAAAGA ATCCCAGGAT TTTCCCTCCT      60
GTGTGTTTTT GTCTTCTTTC TTCATGGTCC ATGATGCCAG CTGAGGTTGT CAGTACAATG      120
AAACCAAACT GGCAGGATG AAGCAOATTA TTCTGCCATT TTTCCAGGTC TTT          173
```

## ( 2 ) INFORMATION FOR SEQ ID NO:5:

- ( i ) SEQUENCE CHARACTERISTICS:  
 ( A ) LENGTH: 197 base pairs  
 ( B ) TYPE: nucleic acid  
 ( C ) STRANDEDNESS: double

-continued

( D ) TOPOLOGY: linear

( i i ) MOLECULE TYPE: DNA (genomic)

( x i ) SEQUENCE DESCRIPTION: SEQ ID NO:5:

```

GGCTGGACAT GGGTGGCCCTC CACGTCCCTC ATATCCCCAG GCACACTCTG GCCTCAGGTT      60
TTGCCCTGGC CATGTCATCT ACCTGGAGTG GGGCCCTCCCC TTCTTCAGCC TTGAATCAAA      120
AGCCACTTTG TTAGGCGAGG ATTTCCAGA CCACTCATCA CATTAAAAAA TATTTTAAAA      180
ACAAAAA      197

```

( 2 ) INFORMATION FOR SEQ ID NO:5:

( i ) SEQUENCE CHARACTERISTICS:

- ( A ) LENGTH: 132 base pairs
- ( B ) TYPE: nucleic acid
- ( C ) STRANDEDNESS: double
- ( D ) TOPOLOGY: linear

( i i ) MOLECULE TYPE: DNA (genomic)

( x i ) SEQUENCE DESCRIPTION: SEQ ID NO:6:

```

TTGACAAAGC TGTTTATTTT CACCAATAAA TAGTATATGG TGATTGGGGT TTCTATTTAT      60
AAGAGTAGTG GCTATTATAT GGGGTATCAT GTTGATGCTC ATAAATAGTT CATATCTACT      120
TAATTTGCCT TC      132

```

( 2 ) INFORMATION FOR SEQ ID NO:7:

( i ) SEQUENCE CHARACTERISTICS:

- ( A ) LENGTH: 75 base pairs
- ( B ) TYPE: nucleic acid
- ( C ) STRANDEDNESS: double
- ( D ) TOPOLOGY: linear

( i i ) MOLECULE TYPE: DNA (genomic)

( x i ) SEQUENCE DESCRIPTION: SEQ ID NO:7:

```

GAAGAGAGTT GTATGTACAA CCCCACACAG CAAGGCAGCT AAATOCAGAG GGTACAGAGA      60
GATCCCGAGG GAATT      75

```

( 2 ) INFORMATION FOR SEQ ID NO:8:

( i ) SEQUENCE CHARACTERISTICS:

- ( A ) LENGTH: 151 base pairs
- ( B ) TYPE: nucleic acid
- ( C ) STRANDEDNESS: double
- ( D ) TOPOLOGY: linear

( i i ) MOLECULE TYPE: DNA (genomic)

( x i ) SEQUENCE DESCRIPTION: SEQ ID NO:8:

```

GGATGGAAC ATGTAGAAAT CCAGAGAAAA ACAATTTTAA AAAAAGGTGG AAAAGTTACG      60
GCAACCTGA GATTTCAGCA TAAAACTTTT AGTTAGAAAT GAGAGAAAGA AGAGGGAGGC      120
TGTTTGCTGT TGCACGTATC AATAGGTTAT C      151

```

( 2 ) INFORMATION FOR SEQ ID NO:9:

( i ) SEQUENCE CHARACTERISTICS:

- ( A ) LENGTH: 141 base pairs
- ( B ) TYPE: nucleic acid
- ( C ) STRANDEDNESS: double
- ( D ) TOPOLOGY: linear

( i i ) MOLECULE TYPE: DNA (genomic)

-continued

## ( 1 ) SEQUENCE DESCRIPTION: SEQ ID NO:9:

TTCTTGATCT TTAGAACACT ATGAATAGGG AAAAAAGAAA AAAGTGTTC AATAAAAAATG	60
TAGGAGCCGT GCTTTTGGAA TGCTTGAGTG AGGAGCTCAA CAAGTCCTCT CCCAAGAAAG	120
CAATGATAAA ACTTGACAAA A	141

## ( 2 ) INFORMATION FOR SEQ ID NO:10:

- ( i ) SEQUENCE CHARACTERISTICS:
- ( A ) LENGTH: 162 base pairs
  - ( B ) TYPE: nucleic acid
  - ( C ) STRANDEDNESS: double
  - ( D ) TOPOLOGY: linear

( i i ) MOLECULE TYPE: DNA (genomic)

## ( 1 ) SEQUENCE DESCRIPTION: SEQ ID NO:10:

ACCCATTTCT AACAAATTTT ACTGTAAAAAT TTTTGGTCAA AGTTCTAAGC TTAATCACAT	60
CTCAAAGAAT AGAGGCAATA TATAGCCCAT CTTACTAGAC ATACAGTATT AAAGTGGACT	120
GAATATGAGG ACAAGCTCTA GTGGTCATTA AACCCCTCAG AA	162

## ( 2 ) INFORMATION FOR SEQ ID NO:11:

- ( i ) SEQUENCE CHARACTERISTICS:
- ( A ) LENGTH: 157 base pairs
  - ( B ) TYPE: nucleic acid
  - ( C ) STRANDEDNESS: double
  - ( D ) TOPOLOGY: linear

( i i ) MOLECULE TYPE: DNA (genomic)

## ( 1 ) SEQUENCE DESCRIPTION: SEQ ID NO:11:

ACATATATTA ACAGCATTCA TTTGGCCAAA ATCTACACGT TTGTAGAATC CTAAGTATTA	60
TAAAGTGGGA ATGTATCAAG TATAGACTAT GAAAGTGCAA ATAACAAATC AAGGTTAAT	120
TAACITTTTT TTTTACATT ATAAAATTAA CTTGTTT	157

## ( 2 ) INFORMATION FOR SEQ ID NO:12:

- ( i ) SEQUENCE CHARACTERISTICS:
- ( A ) LENGTH: 75 base pairs
  - ( B ) TYPE: nucleic acid
  - ( C ) STRANDEDNESS: double
  - ( D ) TOPOLOGY: linear

( i i ) MOLECULE TYPE: DNA (genomic)

## ( 1 ) SEQUENCE DESCRIPTION: SEQ ID NO:12:

CCAAATTTCT CTGGAATCCA TCCTCCCTCC CATCACCATA GCCTCGAGAC GTCATTTCTG	60
TTTGACTACT CCAGC	75

## ( 2 ) INFORMATION FOR SEQ ID NO:13:

- ( i ) SEQUENCE CHARACTERISTICS:
- ( A ) LENGTH: 124 base pairs
  - ( B ) TYPE: nucleic acid
  - ( C ) STRANDEDNESS: double
  - ( D ) TOPOLOGY: linear

( i i ) MOLECULE TYPE: DNA (genomic)

## ( 1 ) SEQUENCE DESCRIPTION: SEQ ID NO:13:

AACTAACCTC CTCGACCCC TGCCTCACTC ATTTACACCA ACCACCCAAC TATCTATAAA	60
CCTGAGCCAT GGCCATCCCT TATGAOCGGC GCAGTGATTA TAGGCTTTTC CTCTAAGATA	120

AAAT

124

## ( 2 ) INFORMATION FOR SEQ ID NO:14:

- ( i ) SEQUENCE CHARACTERISTICS:  
 ( A ) LENGTH: 151 base pairs  
 ( B ) TYPE: nucleic acid  
 ( C ) STRANDEDNESS: double  
 ( D ) TOPOLOGY: linear

( i i ) MOLECULE TYPE: DNA (genomic)

( x i ) SEQUENCE DESCRIPTION: SEQ ID NO:14:

```
ATTATTATTC TTTTTTTATG TTAGCTTAGC CATGCAAAAT TTACTGGTGA AGCAGTTAAT      60
AAAACACACA TCCCATTGAA GGGTTTTGTA CATTTCAGTC CTTACAAATA ACAAAGCAAT      120
GATAAACCCG GCACGTCCTG ATAGGAAATT C                                     151
```

## ( 2 ) INFORMATION FOR SEQ ID NO:15:

- ( i ) SEQUENCE CHARACTERISTICS:  
 ( A ) LENGTH: 105 base pairs  
 ( B ) TYPE: nucleic acid  
 ( C ) STRANDEDNESS: double  
 ( D ) TOPOLOGY: linear

( i i ) MOLECULE TYPE: DNA (genomic)

( x i ) SEQUENCE DESCRIPTION: SEQ ID NO:15:

```
CGTGACACAA ACATGCATTC GTTTTATTCA TAAACAGCC TGGTTTCCTA AAACAATACA      60
AACAGCATGT TCATCAOCAG GAAGCTGCC GTGGGCAGGG GGGCC                                     105
```

## ( 2 ) INFORMATION FOR SEQ ID NO:16:

- ( i ) SEQUENCE CHARACTERISTICS:  
 ( A ) LENGTH: 246 base pairs  
 ( B ) TYPE: nucleic acid  
 ( C ) STRANDEDNESS: double  
 ( D ) TOPOLOGY: linear

( i i ) MOLECULE TYPE: DNA (genomic)

( x i ) SEQUENCE DESCRIPTION: SEQ ID NO:16:

```
ATAAGTTAGA TTCTATTCA CCGGACTAGT TAGCTTTAAG CACCCTAGAG GACTAGGGTA      60
ATCTGACTTC TCACTTCCTA AGTTCCCTCT TATATECTCA AGGTAGAAAT GTCTATGTT      120
TCTACTCCAA TTCATAAATC TATTCATAAG TCTTTGGTAC AAGTTACATG ATAAAAAGAA      180
ATGTGATTTG TCTTCCCTTC TTTGCACTTT TGAATAAAG TATTTATCTC CTOTCTACAG      240
T.TTAAT                                     246
```

## ( 2 ) INFORMATION FOR SEQ ID NO:17:

- ( i ) SEQUENCE CHARACTERISTICS:  
 ( A ) LENGTH: 188 base pairs  
 ( B ) TYPE: nucleic acid  
 ( C ) STRANDEDNESS: double  
 ( D ) TOPOLOGY: linear

( i i ) MOLECULE TYPE: DNA (genomic)

( x i ) SEQUENCE DESCRIPTION: SEQ ID NO:17:

```
GTCCAGTATA AAGGAAAGCG TTAAGTCOGT AAGCTAGAGG ATTGTAAATA TCTTTTATGT      60
CCTCTAGATA AAACACCCGA TTAACAGATG TTAACCTTTT ATGTTTTGAT TCGCTTTAAA      120
AATGGCCTTC TACACATTAG CTCCAGCTAA AAAGACACAT TGAGAGCTTA GAGGATAGTC      180
```

-continued

TCTGGAGC

188

## ( 2 ) INFORMATION FOR SEQ ID NO:18:

- ( 1 ) SEQUENCE CHARACTERISTICS:  
 ( A ) LENGTH: 212 base pairs  
 ( B ) TYPE: nucleic acid  
 ( C ) STRANDEDNESS: double  
 ( D ) TOPOLOGY: linear

( 1.1 ) MOLECULE TYPE: DNA (genomic)

( 2.1 ) SEQUENCE DESCRIPTION: SEQ ID NO:18:

```
GCACCTTGGAA OGGAGTTGGT GTGCTATTTT TGAACACAGAT GTGOTOATAC TGAGATTGTC      60
TGTTTCAGTTT CCCCATTGTG TTGTGCTTCA AATGATCCTT CCTACTTTGC TTCTCTCCAC      120
CCATGACCTT TTTCACTGTG GCCATCAAGG ACTTTCTCTGA CAGCTTGTTGT ACTCTTAGGC      180
TAAGAGATGT GACTACAGCC TGCCCTGAC TO                                     212
```

## ( 2 ) INFORMATION FOR SEQ ID NO:19:

- ( 1 ) SEQUENCE CHARACTERISTICS:  
 ( A ) LENGTH: 203 base pairs  
 ( B ) TYPE: nucleic acid  
 ( C ) STRANDEDNESS: double  
 ( D ) TOPOLOGY: linear

( 1.1 ) MOLECULE TYPE: DNA (genomic)

( 2.1 ) SEQUENCE DESCRIPTION: SEQ ID NO:19:

```
TGTTAGTTTT TAGGAAGGCC TOTCTTCTGG GAGTGAGGTT TATTAGTCCA CTTCTTOGAG      60
CTAGACGTCC TATAGTTAGT CACTGGGGAT GGTGAAAGAG GGAGAAGAGG AAGGGCGAAG      120
GGAAGGGCTC TTTGCTAGTA TCTCCATTTC TAGAAGATGG TTTAGATGAT AACCACAGGT      180
CTATATGAGC ATAGTAAGGC TGT                                           203
```

## ( 2 ) INFORMATION FOR SEQ ID NO:20:

- ( 1 ) SEQUENCE CHARACTERISTICS:  
 ( A ) LENGTH: 177 base pairs  
 ( B ) TYPE: nucleic acid  
 ( C ) STRANDEDNESS: double  
 ( D ) TOPOLOGY: linear

( 1.1 ) MOLECULE TYPE: DNA (genomic)

( 2.1 ) SEQUENCE DESCRIPTION: SEQ ID NO:20:

```
CCTATTTCTG ATCCTGACTT TGGACAAGGC CCTTCAAGCA GAAGACTGAC AAAGTCATCC      60
TCCGTCTACC AGAGCGTGCA CTGTGATCC TAAAATAAGC TTCATCTCCG GCTGTGCCTT      120
GGGTGGAAGG GGCAGGATTC TGCAGCTGCT TTTGCATTTC TCTTCCTAAA TTTCATT      177
```

## ( 2 ) INFORMATION FOR SEQ ID NO:21:

- ( 1 ) SEQUENCE CHARACTERISTICS:  
 ( A ) LENGTH: 106 base pairs  
 ( B ) TYPE: nucleic acid  
 ( C ) STRANDEDNESS: double  
 ( D ) TOPOLOGY: linear

( 1.1 ) MOLECULE TYPE: DNA (genomic)

( 2.1 ) SEQUENCE DESCRIPTION: SEQ ID NO:21:

```
CGGAGCGTAG GTGTGTTTAT TCCTGTACAA ATCATTACAA AACCAAGTCT GGGGCAGTCA      60
CGGCCCCCAC CCATCACCCC AOTGCAATGG CTAGCTGCTG GCCTTT                    106
```

-continued

## ( 2 ) INFORMATION FOR SEQ ID NO:22:

## ( i ) SEQUENCE CHARACTERISTICS:

- ( A ) LENGTH: 139 base pairs
- ( B ) TYPE: nucleic acid
- ( C ) STRANDEDNESS: double
- ( D ) TOPOLOGY: linear

## ( i i ) MOLECULE TYPE: DNA (genomic)

## ( x i ) SEQUENCE DESCRIPTION: SEQ ID NO:22:

```
TTAATTCAAT CAAAACAAGC AACCCCTTT GGCCTGCTG CCACTGGGT CATGCGGTT      60
GTGGCAGCTG GAGAGGTTT CCAACACCC TCCTCTGCTT CCCTGTGTGT CCGGGTCTCA    120
GGAGCTOACC CAGAGTGGG                                     139
```

## ( 2 ) INFORMATION FOR SEQ ID NO:23:

## ( i ) SEQUENCE CHARACTERISTICS:

- ( A ) LENGTH: 177 base pairs
- ( B ) TYPE: nucleic acid
- ( C ) STRANDEDNESS: double
- ( D ) TOPOLOGY: linear

## ( i i ) MOLECULE TYPE: DNA (genomic)

## ( x i ) SEQUENCE DESCRIPTION: SEQ ID NO:23:

```
GCTGAATGTT TAAGAGAGAT TTGGTCTTA AAGGCTTCAT CATGAAAGTG TACATGCATA      60
TGCAAGTGTG AATTACGTGG TATGGATGGT TGCTTGTITA TTAATAAAG ATGTACAGCA    120
AACTGCCCCG TTAGAGTCCT CTTAATATG ATGTCCTAAC ACTGGGTCTG CTTATGC      177
```

## ( 2 ) INFORMATION FOR SEQ ID NO:24:

## ( i ) SEQUENCE CHARACTERISTICS:

- ( A ) LENGTH: 167 base pairs
- ( B ) TYPE: nucleic acid
- ( C ) STRANDEDNESS: double
- ( D ) TOPOLOGY: linear

## ( i i ) MOLECULE TYPE: DNA (genomic)

## ( x i ) SEQUENCE DESCRIPTION: SEQ ID NO:24:

```
GCCAGTGGGA TATGAAATCC AGAAGGGAAA CAAGCACTGG ATAATTAAAA ACACTGGGG      60
AGAAAACTGG GGAACAAAAG GATATATCCT CATGGCTCGA AATAAGAACA ACGCCTGTGG    120
CATTGCCAAC CTGCCAGCT TCCCAAGAT GTGACTCCAG CCAGAAA      167
```

## ( 2 ) INFORMATION FOR SEQ ID NO:25:

## ( i ) SEQUENCE CHARACTERISTICS:

- ( A ) LENGTH: 151 base pairs
- ( B ) TYPE: nucleic acid
- ( C ) STRANDEDNESS: double
- ( D ) TOPOLOGY: linear

## ( i i ) MOLECULE TYPE: DNA (genomic)

## ( x i ) SEQUENCE DESCRIPTION: SEQ ID NO:25:

```
GCCAGGGCGG ACCCTCTTTA TTCCTCTCCT GCCTCAGAGG TCAGGAAGGA GGTCTGGCAG      60
GACCTGCAGT GGGCCCTAGT CATCTGTGGC AGCGAAAGTG AAGGGACTCA CCTGTGCGCC    120
COTGCCTGAG TAGAATTGT TCTGGAATTC C                                     151
```

## ( 2 ) INFORMATION FOR SEQ ID NO:26:

## ( i ) SEQUENCE CHARACTERISTICS:

-continued

( A ) LENGTH: 156 base pairs  
 ( B ) TYPE: nucleic acid  
 ( C ) STRANDEDNESS: double  
 ( D ) TOPOLOGY: linear

( i i ) MOLECULE TYPE: DNA (genomic)

( x i ) SEQUENCE DESCRIPTION: SEQ ID NO:26:

AACTCTTTCA CACTCTGGTA TTTTATGTTT AACAAATATAT GTGTGTGTGC TTGGAAATTA 60  
 GTTCATATCA ATTCATATTG AGCTGTCTCA TTCTTTTTTTT AATGGTCATA TACAGTAGTA 120  
 TTCAATTATA AGAATATATC CTAATACTTT TTAATAA 156

( 2 ) INFORMATION FOR SEQ ID NO:27:

( i ) SEQUENCE CHARACTERISTICS:

( A ) LENGTH: 150 base pairs  
 ( B ) TYPE: nucleic acid  
 ( C ) STRANDEDNESS: double  
 ( D ) TOPOLOGY: linear

( i i ) MOLECULE TYPE: DNA (genomic)

( x i ) SEQUENCE DESCRIPTION: SEQ ID NO:27:

GGATAAGAAA GAAGGCCTGA GGCTAGGGG CCGGGGCTGG CCTGCGTCTC AGTCCTGGGA 60  
 CGCAGCAGCC CGCACAGTT GAGAGGGGCA CTCCTCTTG CTTAGGTTGG TGAGGATCTG 120  
 GTCCTGGTTG GCCGGTGGAG AGCCACAAAA 150

( 2 ) INFORMATION FOR SEQ ID NO:28:

( i ) SEQUENCE CHARACTERISTICS:

( A ) LENGTH: 212 base pairs  
 ( B ) TYPE: nucleic acid  
 ( C ) STRANDEDNESS: double  
 ( D ) TOPOLOGY: linear

( i i ) MOLECULE TYPE: DNA (genomic)

( x i ) SEQUENCE DESCRIPTION: SEQ ID NO:28:

GCACCTGGAA GGGAGTTGGT GTGCTATTTT TGAAGCAGAT GTGGTGATAC TGAGATTGTC 60  
 TGTTCAAGTT CCCCATTTGT TTGTCTTCA AATGATCCTT CCTACTTTGC TTCTCTCCAC 120  
 CCATGACCTT TTCACTGTG GCCATCAAGG ACTTTCCTGA CAGCTTGTGT ACTCTTAGGC 180  
 TAAGAGATGT GACTACAGCC TGCCCTGAC TG 212

( 2 ) INFORMATION FOR SEQ ID NO:29:

( i ) SEQUENCE CHARACTERISTICS:

( A ) LENGTH: 157 base pairs  
 ( B ) TYPE: nucleic acid  
 ( C ) STRANDEDNESS: double  
 ( D ) TOPOLOGY: linear

( i i ) MOLECULE TYPE: DNA (genomic)

( x i ) SEQUENCE DESCRIPTION: SEQ ID NO:29:

ATCCCTGGCT GTGGATAGTG CTTTGTGTA GCAAATGCTC CCTCCTTAAG GTTATAGGGC 60  
 TCCCTGAGTT TGGGAGTGTG GAACTACTAC TTAAGTGTCT GTCCTGCTTG GCTGTCGTTA 120  
 TCGTTTTCTG GTGATGTTGT GCTAACAATA AGAATAC 157

( 2 ) INFORMATION FOR SEQ ID NO:30:

( i ) SEQUENCE CHARACTERISTICS:

( A ) LENGTH: 152 base pairs  
 ( B ) TYPE: nucleic acid



-continued

( C ) STRANDEDNESS: double  
( D ) TOPOLOGY: linear

( i i ) MOLECULE TYPE: DNA (genomic)

( x i ) SEQUENCE DESCRIPTION: SEQ ID NO:30:

```
GGCTGGGCAT CCCTCTCCTC CTCCATCCCC ATACATCACC AGGTCTAATG TTTACAAACG      60
GTCCAGCCCC GGCTCTGAAG CCAAGGGCCG TCCGTGCCAC GGTGGCTGTG AGTATTCCTC      120
CGTTAGCTTT CCCATAAGGT TGGAGTATCT GC                                  152
```

( 2 ) INFORMATION FOR SEQ ID NO:31:

( i ) SEQUENCE CHARACTERISTICS:

( A ) LENGTH: 90 base pairs  
( B ) TYPE: nucleic acid  
( C ) STRANDEDNESS: double  
( D ) TOPOLOGY: linear

( i i ) MOLECULE TYPE: DNA (genomic)

( x i ) SEQUENCE DESCRIPTION: SEQ ID NO:31:

```
CCAACCTCTA CCOCGATACA GACCCACAGA GTGCCATCCC TGAGAGACCA GACCGCTCCC      60
CAATACTCTC CTAAAAATAA CATGAAGCAC                                  90
```

( 2 ) INFORMATION FOR SEQ ID NO:32:

( i ) SEQUENCE CHARACTERISTICS:

( A ) LENGTH: 43 base pairs  
( B ) TYPE: nucleic acid  
( C ) STRANDEDNESS: double  
( D ) TOPOLOGY: linear

( i i ) MOLECULE TYPE: DNA (genomic)

( x i ) SEQUENCE DESCRIPTION: SEQ ID NO:32:

```
CATGGATGAA TGTCTCATGG TGGGAAGGAA CATGATACAT TTC                        43
```

( 2 ) INFORMATION FOR SEQ ID NO:33:

( i ) SEQUENCE CHARACTERISTICS:

( A ) LENGTH: 2333 base pairs  
( B ) TYPE: nucleic acid  
( C ) STRANDEDNESS: double  
( D ) TOPOLOGY: linear

( i i ) MOLECULE TYPE: DNA (genomic)

( x i ) SEQUENCE DESCRIPTION: SEQ ID NO:33:

```
AGACACCTCT GCCCTCACCA TGAGCCTCTG GCAGCCCTTG GTCCTGCTGC TCCTGTGCTC      60
GGGCTGCTGC TTTGCTGCCC CCAGACAGCG CCAGTCCACC CTTGTGCTCT TCCCTGGAGA      120
CCTGAGAACC AATCTCACCG ACAGGCAGCT GGCAGAGGAA TACCTGTACC GCTATGTTA      180
CACTCGGGTG GCAGAGATGC GTGAGAGGTC GAAATCTCTG GGGCCTGCGC TGCTGCTTCT      240
CCAGAAGCAA CTCTCCCTGC CCGAGACCGG TGAAGCTGAT AGCGCCACGC TGAAAGCCAT      300
GCGAACCCCA CGGTGCGGGG TCCCAGACCT GGGCAGATTC CAAACCTTTG AGGCGGACCT      360
CAAATGGCAC CACCACAACA TCACCTATTG GATCCAAAAC TACTCGGAAG ACTTGCCGCG      420
GGCGGTGATT GACGACGCCT TTGCCCGCGC CTTGCGACTG TGGAGCGCGG TGACGCCGCT      480
CACCTTCACT CCGGTGTACA GCCGGGACGC AGACATCGTC ATCCAGTTTG GTGTGCGGGA      540
GCACGGAGAC GGGTATCCCT TCGACGGGAA GGACGGGCTC CTGGCACACG CCTTTCCTCC      600
TGCCCCCGGC ATTACGGGAG ACGCCCATTT CGACGATGAC GAGTTGTGGT CCCTGGGCAA      660
```

-continued

GGGCOTCGTG	GTTCCAAC	TG	GGTGGAAA	CGCAGATGGC	GCGGCCTGCC	ACTTCCCCTT	720
CATCTTTCGAG	GGCCGCTCCT	ACTCTGCCTG	CACCACCGAC	GGTCGCTCCG	ACGGGTTCGC		780
CTGGTGCAAT	ACCACGGCCA	ACTACGACAC	CGACGACCGG	TTTGCTTCT	GCCCCAGCGA		840
GAGACTCTAC	ACCCGGGACG	GCAATGCTGA	TGGGAAACCC	TGCCAGTTTC	CATTCTCTT		900
CCAAGGCCAA	TCCTACTCCG	CCTGCACCAC	GGACGGTCGC	TCCGACGGCT	ACCGCTGGTG		960
CGCCACCACC	GCCAACTACG	ACCGGGACAA	GCTCTTCGGC	TTCTGCCCCG	CCCGAGCTGA		1020
CTCGACGGTG	ATGGGGGGCA	ACTCGGCGGG	GGAGCTGTGC	GTCTTCCCCT	TCACTTTCCT		1080
GGGTAAGGAG	TACTCGACCT	GTACCAGCGA	GGGCCGCGGA	GATGGGCGCC	TCTGOTGCGC		1140
TACCACCTCG	AACTTTGACA	GCGACAAGAA	GTGGGCTTTC	TGCCCCGACC	AAGGATACAG		1200
TTTGTTCCTC	GTGGCGGGCG	ATGAGTTTCG	CCACGCGCTG	GGCTTAGATC	ATTCTCAGT		1260
CCCGGAGGCG	CTCATGTACC	CTATGTACCG	CTTCACTGAG	GGCCCCCCT	TGCATAAGGA		1320
CGACGTGAAT	GGCATCCGGC	ACCTCTATGG	TCCTCGCCCT	GAACCTGAAC	CACGGCCTCC		1380
AACCACCACC	ACACCGCAGC	CCACGGCTCC	CCCGACGGTC	TGCCCCACCG	GACCCCCCAC		1440
TGTCCACCCC	TCAGAGCGCC	CCACAGCTGG	CCCCACAGGT	CCCCCTCAG	CTGGCCCCAC		1500
AGGTCCCCCC	ACTGCTGGCC	CTTCTACGGC	CACTACTGTG	CCTTTGAGTC	CGGTGGACGA		1560
TGCCTGCAAC	GTGAACATCT	TCGACGCCAT	CGCGGAGATT	GGGAACCAGC	TGTATTTGTT		1620
CAAGGATGGG	AAGTACTGGC	GATTCTCTGA	GGGCAAGGGG	AAGCGGCCGC	AGGGCCCCCT		1680
CCTTATCGCC	GACAAGTGGC	CCGCGCTGCC	CCGCAAGCTG	GACTCGGTCT	TTGAGGAGCC		1740
GCTCTCCAAG	AAGCTTTTCT	TCTTCTCTGG	CGCCAGGTG	TGGGTGTACA	CAGGCGCGTC		1800
GGTGCTGGGC	CCGAGGCGTC	TGGACAAGCT	GGGCTGGGA	GCCGACGTGG	CCCAGGTGAC		1860
CGGGGCCCTC	CGGAGTGGCA	GGGGGAAGAT	GCTGCTGTTT	AAGCGGCGGC	GCCTCTGGAG		1920
GTTCGACGTG	AAGGCGCAQA	TGGTGGATCC	CCGGAGCGCC	AACGAGGTGG	ACCGGATGTT		1980
CCCCGGGGTG	CCTTTGGACA	CGCAGGACGT	CTTCCAGTAC	CGAGAGAAAG	CCTATTTCTG		2040
CCAGGACCGC	TTCTACTGGC	CGGTGAGTTC	CCGGAGTGAG	TTGAACCAGG	TGGACCAAT		2100
GGGCTACGTG	ACCTATGACA	TCCTGCAGTG	CCCTGAGGAC	TAGGGCTCCC	GTCTGTCTTT		2160
GCAGTGCCAT	GTAATCCCC	ACTGGGACCA	ACCCTGGGGA	AAGAGCCAGT	TTGCCGGATA		2220
CAAACTGGTA	TTCTGTTCTG	GAGGAAAGGG	AGGAGTGGAG	GTGGGCTGGG	CCCTCTCTTC		2280
TCACCTTTGT	TTTTTGTGG	AGTGTCTCTA	ATAAACTTGG	ATTCTCTAAC	CTTT		2334

## (2) INFORMATION FOR SEQ ID NO:34:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

## (ii) MOLECULE TYPE: peptide

## (iii) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Glu Ala Leu Met Tyr Pro Met Tyr Arg Phe Thr Glu Gly Pro Pro Leu  
 1 5 10 15

His Lys

## We claim:

1. An isolated osteoclast-specific or -related DNA sequence, or its complementary sequence, the DNA 65 sequence comprising a nucleic acid sequence selected from the group consisting of:

a) DNA sequences set forth in the group consisting of SEQ ID NOS. 12, 14, 16 and 17, or their complementary strands; and

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- b) DNA sequences which hybridize under standard conditions to the DNA sequences defined in a).
2. A DNA construct capable of replicating, in a host cell, osteoclast-specific or -related DNA, said construct comprising:
- a) a DNA sequence of claim 1; and
- b) sequences, in addition to said DNA sequence, necessary for transforming or transfecting a host cell, and for replicating, in a host cell, said DNA sequence.
3. A DNA construct capable of replicating and expressing, in a host cell, osteoclast-specific or -related DNA, said construct comprising:

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- a) a DNA sequence of claim 2; and
- b) sequences, in addition to said DNA sequence, necessary for transforming or transfecting a host cell, and for replicating and expressing, in a host cell, said DNA sequence.
4. A cell stably transformed or transfected with a DNA construct according to claim 3.
5. A cell stably transformed or transfected with a DNA construct according to claim 4.

\* \* \* \* \*